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TECH CENTER 1600/2900



1600

p#12

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,340A

DATE: 07/25/2002

TIME: 08:40:21

Input Set : A:\501d4.app

Output Set: N:\CRF3\07252002\I647340A.raw

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AUG 15 2002

TECH CENTER 1600/2900

ENTERED

4 <110> APPLICANT: Brunkow, Mary E.
 5 Jeffery, Eric W.
 6 Hjerrild, Kathryn A.
 7 Ramsdell, Fred
 11 <120> TITLE OF INVENTION: IDENTIFICATION OF THE GENE CAUSING THE
 12 MOUSE SCURFY PHENOTYPE AND ITS HUMAN ORTHOLOG
 15 <130> FILE REFERENCE: 240083.501D4
 C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/647,340A
 18 <141> CURRENT FILING DATE: 2000-10-24
 20 <160> NUMBER OF SEQ ID NOS: 14
 22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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 25 <211> LENGTH: 2160
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Mus musculus
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 32 caccagtaca gctggaaaca ccagccact ccagctcccg gcaacttctc ctgactctgc 180
 33 cttcagacga gacttggaag acagtcacat ctacgagct cctctgccgt tatccagcct 240
 34 gcctctgaca agaacccaat gcccaaccct aggccagcca agcctatggc tccttccctg 300
 35 gcccttgccc catccccagg agtcttgcca agctggaaga ctgcacccaa gggctcagaa 360
 36 cttctagggg ccaggggctc tgggggaccc ttccaaggtc gggacctgcg aagtggggcc 420
 37 cacacctctt ctctcttgaa ccccttgcca ccattccagc tgcagctgcc tacagtgcc 480
 38 ctagtcatgg tggcacctgc tggggcccga ctaggctcct caccacacct acaggccctt 540
 39 ctccaggaca gaccacactt catgcatcag ctctccactg tggatgcca tgcccagacc 600
 40 cctgtgctcc aagtgcgtcc actggacaac ccagccatga tcagcctccc accaccttct 660
 41 gctgccactg gggctcttct cctcaaggcc cggcctggcc tgccacctgg gatcaatgtg 720
 42 gccagtctgg aatgggtgtc cagggagcca gctctactct gcaccttccc acgctcgggt 780
 43 acaccagga aagacagcaa ccttttggtt gcaccccaag gatcctaccc actgctggca 840
 44 aatggagtct gcaagtggcc tggttgtgag aaggtcttcg aggagccaga agagtttctc 900
 45 aagcactgcc aagcagatca tctcctggat gagaaaggca aggccagtg cctcctccag 960
 46 agagaagtgg tgcagtctct ggagcagcag ctggagctgg aaaaggagaa gctgggagct 1020
 47 atgcaggccc acctggctgg gaagatggcg ctggccaagg ctccatctgt ggctcaatg 1080
 48 gacaagagct cttgctgcac cgtagccacc agtactcagg gcagtgtgct cccggcctgg 1140
 49 tctgctctcc tggaggctcc agacggcgcc ctgtttgcag tgcggaggca cctctgggga 1200
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 53 agaaaccacc ccgccacctg gaagaatgcc atccgccaca acctgagcct gcacaagtgc 1440
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59 tcccagccta gccctagtt ccaacctagc cccaagatga actttccagt caaagagccc 1800
60 tcacaaccag ctatacatat ctgccttggc cactgccaaag cagaaagatg acagacacca 1860
61 tcctaataatt tactcaaccc aaaccctaaa acatgaagag cctgccttgg tacattcgtg 1920
62 aactttcaaaa gttagtcagt cagtcacaca tgactgcagt cctactgact cacaccccaa 1980
63 agcactcacc cacaacatct ggaaccacgg gcactatcac acataggtgt atatacagac 2040
64 ccttacacag caacagcact ggaaccttca caattacatc cccccaaacc acacaggcat 2100
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68 <211> LENGTH: 429
69 <212> TYPE: PRT
70 <213> ORGANISM: Mus musculus
72 <400> SEQUENCE: 2
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75 Gly Pro Ser Pro Gly Val Leu Pro Ser Trp Lys Thr Ala Pro Lys Gly
76 20 25 30
77 Ser Glu Leu Leu Gly Thr Arg Gly Ser Gly Gly Pro Phe Gln Gly Arg
78 35 40 45
79 Asp Leu Arg Ser Gly Ala His Thr Ser Ser Ser Leu Asn Pro Leu Pro
80 50 55 60
81 Pro Ser Gln Leu Gln Leu Pro Thr Val Pro Leu Val Met Val Ala Pro
82 65 70 75 80
83 Ser Gly Ala Arg Leu Gly Pro Ser Pro His Leu Gln Ala Leu Leu Gln
84 85 90 95
85 Asp Arg Pro His Phe Met His Gln Leu Ser Thr Val Asp Ala His Ala
86 100 105 110
87 Gln Thr Pro Val Leu Gln Val Arg Pro Leu Asp Asn Pro Ala Met Ile
88 115 120 125
89 Ser Leu Pro Pro Pro Ser Ala Ala Thr Gly Val Phe Ser Leu Lys Ala
90 130 135 140
91 Arg Pro Gly Leu Pro Pro Gly Ile Asn Val Ala Ser Leu Glu Trp Val
92 145 150 155 160
93 Ser Arg Glu Pro Ala Leu Leu Cys Thr Phe Pro Arg Ser Gly Thr Pro
94 165 170 175
95 Arg Lys Asp Ser Asn Leu Leu Ala Ala Pro Gln Gly Ser Tyr Pro Leu
96 180 185 190
97 Leu Ala Asn Gly Val Cys Lys Trp Pro Gly Cys Glu Lys Val Phe Glu
98 195 200 205
99 Glu Pro Glu Glu Phe Leu Lys His Cys Gln Ala Asp His Leu Leu Asp
100 210 215 220
101 Glu Lys Gly Lys Ala Gln Cys Leu Leu Gln Arg Glu Val Val Gln Ser
102 225 230 235 240
103 Leu Glu Gln Gln Leu Glu Leu Glu Lys Glu Lys Leu Gly Ala Met Gln
104 245 250 255
105 Ala His Leu Ala Gly Lys Met Ala Leu Ala Lys Ala Pro Ser Val Ala
106 260 265 270
107 Ser Met Asp Lys Ser Ser Cys Cys Ile Val Ala Thr Ser Thr Gln Gly

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Input Set : A:\501d4.app

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108	275	280	285	
109	Ser Val Leu Pro Ala Trp	Ser Ala Pro Arg Glu	Ala Pro Asp Gly Gly	
110	290	295	300	
111	Leu Phe Ala Val Arg Arg	His Leu Trp Gly Ser	His Gly Asn Ser Ser	
112	305	310	315	320
113	Phe Pro Glu Phe Phe His	Asn Met Asp Tyr Phe	Lys Tyr His Asn Met	
114	325/	330	335	
115	Arg Pro Pro Phe Thr Tyr	Ala Thr Leu Ile Arg	Trp Ala Ile Leu Glu	
116	340	345	350	
117	Ala Pro Glu Arg Gln Arg	Thr Leu Asn Glu Ile	Tyr His Trp Phe Thr	
118	355	360	365	
119	Arg Met Phe Ala Tyr Phe	Arg Asn His Pro Ala	Thr Trp Lys Asn Ala	
120	370	375	380	
121	Ile Arg His Asn Leu Ser	Leu His Lys Cys Phe	Val Arg Val Glu Ser	
122	385	390	395	400
123	Glu Lys Gly Ala Val Trp	Thr Val Asp Glu Phe	Glu Phe Arg Lys Lys	
124	405	410	415	
125	Arg Ser Gln Arg Pro Asn	Lys Cys Ser Asn Pro	Cys Pro	
126	420	425		
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129	<211> LENGTH: 1869			
130	<212> TYPE: DNA			
131	<213> ORGANISM: Homo sapien			
133	<400> SEQUENCE: 3			
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135	cgtacagcgt ggtttttctt ctcggtataa	aagcaaagtt gtttttgata cgtgacagtt	120	
136	tcccacaagc caggctgata cttttctgtc	agtccacttc accaagcctg cccttgga	180	
137	aggaccgat gcccaacccc aggcctggca	agccctcggc cccttccttg gcccttg	240	
138	catccccagg agcctcgccc agctggagg	ctgcacccaa agcctcagac ctgctgggg	300	
139	cccggggccc agggggaacc ttccagggcc	gagatcttcg aggcggggcc catgcctc	360	
140	cttcttcctt gaaccccatg ccaccatcgc	agctgcagct gccacactg cccctagtca	420	
141	tgggtggcacc ctccggggca cggctgggcc	ccttgcccca cttacaggca ctccctcagg	480	
142	acaggccaca ttcatgcac cagctctcaa	cgggtgatgc ccacgcccgg acccctgtgc	540	
143	tgcaggtgca cccctggag agcccagcca	tgatcagcct cacaccacc accaccgcca	600	
144	ctggggtctt ctccctcaag gcccggcctg	gcctcccacc tgggatcaac gtggccagcc	660	
145	tggaatgggt gtccaggag ccggcactgc	tctgcacctt cccaaatccc agtgaccca	720	
146	ggaaggacag caccctttcg gctgtgcccc	agagctccta cccactgctg gcaaatggtg	780	
147	tctgcaagtg gcccgatgt gagaaggtct	tcgaagagcc agaggacttc ctcaagcact	840	
148	gccaggcgga catctttctg gatgagaagg	gcagggcaca atgtctctc cagagagaga	900	
149	tggtagagtc tctggagcag cagctggtgc	tggagaagga gaagctgagt gccatgcagg	960	
150	cccacctggc tgggaaaatg gcaactgacca	aggttcac tgtggcatca tccgacaagg	1020	
151	gctcctgctg catcgtagct gctggcagcc	aaggccctgt cgtcccagcc tggctggcc	1080	
152	cccgggaggc cctgcagc ctgtttgctg	tccggaggca cctgtggggt agccatggaa	1140	
153	acagcacatt cccagagttc ctccacaaca	tggactactt caagttccac aacatgcgac	1200	
154	cccctttcac ctacgccag ctcatccgct	gggccatcct ggaggctcca gagaagcagc	1260	
155	ggacactcaa tgagatctac cactggttca	cacgcatgtt tgctttcttc agaaaccatc	1320	
156	ctgccacctg gaagaacgcc atccgccaca	acctgagtct gcacaagtgc tttgtgcggg	1380	
157	tggagagcga gaagggggt gtgtggaccg	tggatgagct ggagttccgc aagaaacgga	1440	
158	gccagaggcc cagcaggtgt tccaacccta	cacctggccc ctgacctcaa gatcaaggaa	1500	

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161  gggcccctgt  tcccccgctg  gcagccaccc  cctcccccat  catatccttt  gcccccaaggc  1680
162  tgctcagagg  ggccccggtc  ctggccccag  cccccacctc  cgccccagac  acacccccca  1740
163  gtcgagccct  gcagccaaac  agagccttca  caaccagcca  cacagagcct  gcctcagctg  1800
164  ctgcacaga  ttacttcagg  gctggaaaag  tcacacagac  acacaaaatg  tcacaatcct  1860
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168 <211> LENGTH: 431
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapien
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176          20          25          30
177  Ser Asp Leu Leu Gly Ala Arg Gly Pro Gly Gly Thr Phe Gln Gly Arg
178          35          40          45
179  Asp Leu Arg Gly Gly Ala His Ala Ser Ser Ser Ser Leu Asn Pro Met
180          50          55          60
181  Pro Pro Ser Gln Leu Gln Leu Pro Thr Leu Pro Leu Val Met Val Ala
182          65          70          75          80
183  Pro Ser Gly Ala Arg Leu Gly Pro Leu Pro His Leu Gln Ala Leu Leu
184          85          90          95
185  Gln Asp Arg Pro His Phe Met His Gln Leu Ser Thr Val Asp Ala His
186          100         105         110
187  Ala Arg Thr Pro Val Leu Gln Val His Pro Leu Glu Ser Pro Ala Met
188          115         120         125
189  Ile Ser Leu Thr Pro Pro Thr Thr Ala Thr Gly Val Phe Ser Leu Lys
190          130         135         140
191  Ala Arg Pro Gly Leu Pro Pro Gly Ile Asn Val Ala Ser Leu Glu Trp
192          145         150         155         160
193  Val Ser Arg Glu Pro Ala Leu Leu Cys Thr Phe Pro Asn Pro Ser Ala
194          165         170         175
195  Pro Arg Lys Asp Ser Thr Leu Ser Ala Val Pro Gln Ser Ser Tyr Pro
196          180         185         190
197  Leu Leu Ala Asn Gly Val Cys Lys Trp Pro Gly Cys Glu Lys Val Phe
198          195         200         205
199  Glu Glu Pro Glu Asp Phe Leu Lys His Cys Gln Ala Asp His Leu Leu
200          210         215         220
201  Asp Glu Lys Gly Arg Ala Gln Cys Leu Leu Gln Arg Glu Met Val Gln
202          225         230         235         240
203  Ser Leu Glu Gln Gln Leu Val Leu Glu Lys Glu Lys Leu Ser Ala Met
204          245         250         255
205  Gln Ala His Leu Ala Gly Lys Met Ala Leu Thr Lys Ala Ser Ser Val
206          260         265         270
207  Ala Ser Ser Asp Lys Gly Ser Cys Cys Ile Val Ala Ala Gly Ser Gln
208          275         280         285
209  Gly Pro Val Val Pro Ala Trp Ser Gly Pro Arg Glu Ala Pro Asp Ser

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210      290      295      300
211 Leu Phe Ala Val Arg Arg His Leu Trp Gly Ser His Gly Asn Ser Thr
212 305      310      315      320
213 Phe Pro Glu Phe Leu His Asn Met Asp Tyr Phe Lys Phe His Asn Met
214      325      330      335
215 Arg Pro Pro Phe Thr Tyr Ala Thr Leu Ile Arg Trp Ala Ile Leu Glu
216      340      345      350
217 Ala Pro Glu Lys Gln Arg Thr Leu Asn Glu Ile Tyr His Trp Phe Thr
218      355      360      365
219 Arg Met Phe Ala Phe Phe Arg Asn His Pro Ala Thr Trp Lys Asn Ala
220      370      375      380
221 Ile Arg His Asn Leu Ser Leu His Lys Cys Phe Val Arg Val Glu Ser
222 385      390      395      400
223 Glu Lys Gly Ala Val Trp Thr Val Asp Glu Leu Glu Phe Arg Lys Lys
224      405      410      415
225 Arg Ser Gln Arg Pro Ser Arg Cys Ser Asn Pro Thr Pro Gly Pro
226      420      425      430

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228 <210> SEQ ID NO: 5

229 <211> LENGTH: 23

230 <212> TYPE: DNA

231 <213> ORGANISM: Artificial Sequence

233 <220> FEATURE:

234 <223> OTHER INFORMATION: Primer for generation of mouse Fkh cDNA

236 <400> SEQUENCE: 5

237 gcagatctcc tgactctgcc ttc

23

239 <210> SEQ ID NO: 6

240 <211> LENGTH: 23

241 <212> TYPE: DNA

242 <213> ORGANISM: Artificial Sequence

244 <220> FEATURE:

245 <223> OTHER INFORMATION: Primer for generation of mouse Fkh cDNA

247 <400> SEQUENCE: 6

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23

250 <210> SEQ ID NO: 7

251 <211> LENGTH: 21

252 <212> TYPE: DNA

253 <213> ORGANISM: Artificial Sequence

255 <220> FEATURE:

256 <223> OTHER INFORMATION: Primer for generation of human Fkh cDNA

258 <400> SEQUENCE: 7

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21

261 <210> SEQ ID NO: 8

262 <211> LENGTH: 21

263 <212> TYPE: DNA

264 <213> ORGANISM: Artificial Sequence

266 <220> FEATURE:

267 <223> OTHER INFORMATION: Primer for generation of human Fkh cDNA

269 <400> SEQUENCE: 8

270 gcaagacagt ggaaacctca c

21

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/647,340A

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Input Set : A:\501d4.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 3,6,9,12,15
Seq#:14; N Pos. 1,7,10,13,16,19